## nggmyets nggeht

## SEQUENCE LISTING

<110> Lee, Se Yong et al. <120> Trehalose Synthase Protein, Gene, Plasmids, Microorganisms, and A Process for Producing Trehalose <130> 1599-0206P US 09/937,215 <140> <141> 2001-09-24 <160> <170> PatentIn version 3.1 <210> <211> 4753 <212> DNA <213> Pseudomonas stutzeri <220> <221> CDS <222> (1537)..(3603)<223> <400> 1 gategetgge gtactgeagg tagageagge geateggeee eeagggegea teggeegget 60 ccgctgtgcc ctgctggttc atgaagcgga cgaagcggcc atcgcggaac cgtggacgcc 120 attegggget gteegggteg eggetgtegg tgagegtgeg ceaeaggteg etgegaaaeg 180 gcggaccgct ccaaagcgcg ccgtggatgg gatcgccgag cagttcgtgc agctcccagg 240 300 aacgttgcga atgcagcgcg ccgaggctca ggccatgcag atacaggcgc ggtcggcgtt 360 cggccggcag ttcggtccag tagccataga tctcggcgaa tagcgcgcgg gccacgtcgc 420 ggccgtagtc ggcctccacc agcagcgcca gcgggctgtt cagataggag tactgcaacg ccacgctggc gatatcgccg tggtgcaggt attccactgc gttcatcgcc gccgggtcga 480 540 tecageeggt aceggtggge gteaceagea ecageacega tegetegaag gegeegetge getgeagete gegeaaggee agaegegeee getggegegg ggtetetgee gegegeagae 600 cgacgtagac gcgaatcggc tcgagcgccg agcggccgct caagacgctg atatccgccg 660 720 ccgacgggcc ggagccgatg aactcgcggc cggtgcggcc cagctcctcc cagcgcagca. 780 acgaggeecg getgeegett tteageggeg aggeeggtgg egeegtetee ggttegatea 840 gggcgtcgta ctgcgcgaag gatgcgtcca gcatgcgcag tgcccgcgcc gccagcacat

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Pro Glu Gly Gly Thr Val Leu Glu Ala Leu Gly Asp Asp Arg Leu Trp 70 75

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Gly Asn Phe Asp Arg Ile Ser Phe Asp Ile Asp Pro Ser Leu Gly Thr 115 120 125

Glu Glu Gln Met Leu Gln Leu Ser Arg Val Ala Ala Ala His Asn Ala 130 135

Ile Val Ile Asp Asp Ile Val Pro Ala His Thr Gly Lys Gly Ala Asp 145 150

Phe Arg Leu Ala Glu Met Ala Tyr Gly Asp Tyr Pro Gly Leu Tyr His 165 170

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Lys Glu Lys His Tyr Ile Val Gly Gln Leu Gln Arg Val Ile Phe Phe 210 215 220

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Glu Gly Gln Pro Ser Leu Asn Trp Leu Asp Pro Thr Phe Ala Ala Gln 260 265 270

Gln Leu Ile Ile Gly Asp Ala Leu His Ala Ile Asp Val Thr Gly Ala 275 280 285

Arg Val Leu Arg Leu Asp Ala Asn Gly Phe Leu Gly Val Glu Arg Arg 290 295 300

Ala Glu Gly Thr Ala Trp Ser Glu Gly His Pro Leu Ser Val Thr Gly 305 310 315 320

Asn Gln Leu Leu Ala Gly Ala Ile Arg Lys Ala Gly Gly Phe Ser Phe 325 330 335

Gln Glu Leu Asn Leu Thr Ile Asp Asp Ile Ala Ala Met Ser His Gly 340 345 350

Gly Ala Asp Leu Ser Tyr Asp Phe Ile Thr Arg Pro Ala Tyr His His 355 360 365

Ala Leu Leu Thr Gly Asp Thr Glu Phe Leu Arg Met Met Leu Arg Glu 370 375 380

Val His Ala Phe Gly Ile Asp Pro Ala Ser Leu Ile His Ala Leu Gln 385 390 395 400 Asn His Asp Glu Phe Thr Leu Glu Leu Val His Phe Trp Thr Leu His 405 410 415

Ala Tyr Asp His Tyr His Tyr Lys Gly Gln Thr Leu Pro Gly Gly His 420 425 430

Leu Arg Glu His Ile Arg Glu Glu Met Tyr Glu Arg Leu Thr Gly Glu 435 440 445

His Ala Pro Tyr Asn Leu Lys Phe Val Thr Asn Gly Val Ser Cys Thr 450 455 460

Thr Ala Ser Val Ile Ala Ala Ala Leu Asn Ile Arg Asp Leu Asp Ala 465 470 475 480

Ile Gly Pro Ala Glu Val Glu Gln Ile Gln Arg Leu His Ile Leu Leu 485 490 495

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Asp Leu Val Gly Ala Leu Pro Leu Ala Pro Glu Gln Val Glu His Leu 515 520 525

Met Gly Asp Gly Asp Thr Arg Trp Ile Asn Arg Gly Gly Tyr Asp Leu 530 540

Ala Asp Leu Ala Pro Glu Ala Ser Val Ser Ala Glu Gly Leu Pro Lys 545 550 555 560

Ala Arg Ser Leu Tyr Gly Ser Leu Ala Glu Gln Leu Gln Arg Pro Gly 565 570 575

Ser Phe Ala Cys Gln Leu Lys Arg Ile Leu Ser Val Arg Gln Ala Tyr 580 585 590

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